

CLAIMS

What is claimed is:

- 1 Sub 22 } 1. A system comprising
2 an isolated nucleic acid having a length of at least 5 base pairs and
3 having a nucleotide sequence that encodes a first protein binding site and a second protein
4 binding site where said first and second protein binding sites are spaced in proximity to each
5 other such that:
6 when said first protein binding site is specifically bound by a protein,
7 said second binding site cannot be bound by a protein that otherwise specifically
8 recognizes and binds said second binding site; and
9 when said second binding site is specifically bound by a protein, said
10 first binding site cannot be bound by a protein that otherwise specifically recognizes
11 and binds said first binding site; and
12 a nucleic acid binding protein that specifically binds said first protein
13 binding site or said second protein binding site.
- 1 2. The composition of claim 1, wherein said nucleic acid is a double-stranded
2 nucleic acid.
- 1 3. The composition of claim 1, wherein said nucleic acid is a
2 deoxyribonucleic acid (DNA).
- 1 4. The composition of claim 1, wherein said first binding site and said second
2 binding site have the same nucleotide sequence.
- 1 5. The composition of claim 4, wherein said first binding site and said second
2 binding site have the nucleotide sequence of SEQ ID NO: 1.
- 1 6. The composition of claim 1, wherein said first binding site or said second
2 binding site is specifically recognized and bound by a protein selected from the group
3 consisting of Fis, and Tus.
- 1 7. The composition of claim 1, wherein said first binding site or said second
2 binding site is bound by EF-tu.

1 8. The composition of claim 1, wherein said first binding site is within 20
2 nucleotides of said second binding site.

1 9. The composition of claim 1, wherein said first binding site is within 11
2 nucleotides of said second binding site

1 10. The composition of claim 8, wherein said first binding site has a strength
2 of at least 2.4 bits as determined by individual information theory.

1 11. The composition of claim 1, wherein the difference in strength between
2 said first protein binding site and said second protein binding site is at least 0 bits as
3 determined by individual information theory.

1 12. The composition of claim 1, further comprising a third protein binding
2 site wherein said third site is in proximity to said first protein binding site or to said second
3 protein binding site such that specific binding of said third binding site with a protein
4 precludes specific protein binding of said first or said second protein binding sites.

1 13. The composition of claim 1, wherein:
2 said first protein binding site is a Fis binding site;
3 said second protein binding site is a Fis binding site; and
4 said binding sites are separated from each other by less than 12
5 nucleotide base pairs.

1 14. The composition of claim 13, wherein said nucleic acid is a
2 deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

1 15. A composition comprising an isolated nucleic acid having a length of at
2 least 5 base pairs and having a nucleotide sequence that encodes a first protein binding site, a
3 second protein binding site, and a third protein binding site where said protein binding sites
4 are spaced in proximity to each other such that:

5 when either said first protein binding site or said third protein binding
6 is specifically bound by a nucleic acid binding protein, said second binding site cannot be
7 bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said
8 second binding site; and

9 where said first protein binding site and said third protein binding site
10 can simultaneously be specifically bound by a nucleic acid binding protein.

1 16. The composition of claim 15, wherein said first protein binding site or
2 said third protein binding site is bound by a nucleic acid binding protein.

1 17. The composition of claim 15, wherein said third protein binding site is
2 bound by a nucleic acid binding protein.

1 18. The composition of claim 17, wherein said binding protein is attached to a
2 gene transactivator.

1 19. The composition of claim 18, wherein said transactivator is a Gal4
2 transactivator.

1 20. The composition of claim 15, further comprising a gene or cDNA under
2 the control of said transactivator.

1 21. The composition of claim 20, further comprising a gene or cDNA under
2 the control of said transactivator.

1 22. The composition of claim 21, wherein said gene is a reporter gene.

1 23. The composition of claim 21, wherein said gene encodes a nucleic acid
2 binding protein.

1 24. The composition of claim 15, wherein said nucleic acid is a double-
2 stranded nucleic acid.

1 25. The composition of claim 15, wherein said nucleic acid is a
2 deoxyribonucleic acid (DNA).

1 26. The composition of claim 15, wherein said first binding site and said third
2 binding site have the same nucleotide sequence.

1 27. The composition of claim 15, wherein said first binding site or said
2 second binding site is specifically recognized and bound by a protein selected from the group
3 consisting of Fis, and Tus.

1 28. The composition of claim 15, wherein said first binding site or said
2 second binding site is bound by EF-tu.

1 29. The composition of claim 15, wherein said first binding site is within 20
2 nucleotides of said second binding site.

1 30. The composition of claim 15, wherein said first binding site is within 11
2 nucleotides of said second binding site.

1 31. The composition of claim 30, wherein said first binding site has a strength
2 of at least 2.4 bits as determined by individual information theory.

1 32. The composition of claim 15, wherein the difference in strength between
2 said first protein binding site and said second protein binding site is at least 0 bits as
3 determined by individual information theory.

1 33. The composition of claim 1, wherein:
2 said first protein binding site is a Fis binding site;
3 said third protein binding site is a Fis binding site..

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1 SUB B4) 34. A composition for the storage of binary information, said composition
2 comprising an isolated nucleic acid having a length of at least 3 base pairs and having a
3 nucleotide sequence that encodes a first protein binding site and a second protein binding site
4 where said first and second protein binding sites are spaced in proximity to each other such
5 that:
6 when said first protein binding site is specifically bound by a protein,
7 said second binding site cannot be bound by a protein that otherwise specifically recognizes
8 and binds said second binding site; and
9 when said second binding site is specifically bound by a protein, said
10 first binding site cannot be bound by a protein that otherwise specifically recognizes and
11 binds said first binding site; and
12 further comprising a nucleic acid binding protein bound to said first
13 protein binding site or said second protein binding site.

1 35. The composition of claim 34, wherein said nucleic acid is a double-
2 stranded nucleic acid.

1 36. The composition of claim 34, wherein said nucleic acid is a
2 deoxyribonucleic acid (DNA).

1 37. The composition of claim 34, wherein said first binding site and said
2 second binding site have the same nucleotide sequence.

1 38. The composition of claim 34, wherein said first binding site or said
2 second binding site is specifically recognized and bound by a protein selected from the group
3 consisting of Fis, and Tus.

1 39. The composition of claim 34, wherein said first binding site is within 20
2 nucleotides of said second binding site.

1 40. The composition of claim 34, wherein said first binding site is within 20
2 nucleotides of said second binding site

1 41. The composition of claim 40, wherein said first binding site has a strength
2 of at least 2.4 bits as determined by individual information theory.

1 ~~SUB 35~~ 42. The composition of claim 34, wherein the difference in strength between
2 said first protein binding site and said second protein binding site is at least 0 bits as
3 determined by individual information theory.

1 43. The composition of claim 34, further comprising a third protein binding
2 site wherein said third site is in proximity said first protein binding site or said second protein
3 binding site such that specific binding of said third binding site with a protein precludes
4 specific protein binding of said first or said second protein binding sites.

1 44. The composition of claim 34, wherein:
2 said first protein binding site is a Fis binding site;
3 said second protein binding site is a Fis binding site; and
4 said binding sites are separated from each other by less than 12
5 nucleotide base pairs.

1 45. The composition of claim 44, wherein said nucleic acid is a
2 deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

1 46. The composition of claim 34, wherein said binding protein is attached to a
2 gene transactivator.

1 47. The composition of claim 46, wherein said transactivator is a Gal4
2 transactivator.

1 48. The composition of claim 46, further comprising a gene or cDNA under
2 the control of said transactivator.

1 49. The composition of claim 48, wherein said gene is a reporter gene.

1 50. The composition of claim 48, wherein said gene encodes a nucleic acid
2 binding protein.

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1 SUB B6) 51. A method of storing information, said method comprising the step of:
2 binding a nucleic acid binding protein to a first protein binding site on
3 a nucleic acid, wherein said nucleic acid has a length of at least 3 base pairs and said nucleic
4 acid encodes said first protein binding site and a second protein binding site where said first
5 and second protein binding sites are spaced in proximity to each other such that:
6 when said first protein binding site is specifically bound by a protein,
7 said second binding site cannot be bound by a protein that otherwise specifically recognizes
8 and binds said second binding site; and
9 when said second binding site is specifically bound by a protein, said
10 first binding site cannot be bound by a protein that otherwise specifically recognizes and
11 binds said first binding site.

1 52. The method of claim 51, further comprising the step of determining which
2 binding site on said nucleic acid is bound by said binding protein.

1 53. The method of claim 51, wherein said nucleic acid is a double-stranded
2 nucleic acid.

1 54. The method of claim 51, wherein said nucleic acid is a deoxyribonucleic
2 acid (DNA).

1 55. The method of claim 51, wherein said first binding site and said second
2 binding site have the same nucleotide sequence.

1 56. The method of claim 55, wherein said first binding site and said second
2 binding site have the nucleotide sequence of SEQ ID NO: 1.

1 57. The method of claim 51, wherein said first binding site or said second
2 binding site is specifically recognized and bound by a protein selected from the group
3 consisting of Fis, EF-tu, and Tus.

1 58. The method of claim 51, wherein said first binding site is within 20
2 nucleotides of said second binding site.

1 59. The method of claim 51, wherein said first binding site is within 11
2 nucleotides of said second binding site

1 60. The method of claim 51, wherein said first binding site has a strength of at
2 least 2.4 bits as determined by individual information theory.

1 ~~Sub B7~~ 61. ~~The method of claim 51, wherein the difference in strength between said~~
2 ~~first protein binding site and said second protein binding site is at least 0 bits as determined~~
3 ~~by individual information theory.~~

1 62. The method of claim 51, wherein:
2 said first protein binding site is a Fis binding site;
3 said second protein binding site is a Fis binding site; and
4 said binding sites are separated from each other by less than 12
5 nucleotide base pairs.

1 ~~Sub B8~~ 63. ~~The composition of claim 13, wherein said nucleic acid is a~~
2 ~~deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.~~

1 64. A method of transforming binary information, said method comprising the
2 steps of:

3 (i) binding a nucleic acid binding protein to an input protein binding
4 site on a first nucleic acid; and

5 (ii) determining whether or not a nucleic acid binding protein can bind
6 to an output protein binding site on a second nucleic acid;

7 wherein said first nucleic acid is an isolated nucleic acid having a
8 length of at least 5 base pairs and having a nucleotide sequence that encodes a first protein
9 binding site, a second protein binding site, and a third protein binding site where said protein
10 binding sites are spaced in proximity to each other such that:

11 when either said first protein binding site or said third protein binding
12 is specifically bound by a nucleic acid binding protein, said second binding site cannot be
13 bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said
14 second binding site; and

15 where said first protein binding site and said third protein binding site
16 can simultaneously be specifically bound by a nucleic acid binding protein.

65. The method of claim 64, wherein said first nucleic acid and said second nucleic acid are the same nucleic acid.

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